

SEQUENCE LISTING

<110> Napier, Johnathan A.
 Sayanova, Olga
 Lazarus, Colin M.
 Qi, Baoxiu
 Heinz, Ernst
 Zank, Thorsten
 Zahringer, Ulrich

<120> Novel method for the production of polyunsaturated fatty acids

<130> 13478-00001-US

<140> US 10/539,891
 <141> 2005-06-17

<150> PCT/EP2003/014054
 <151> 2003-12-11

<150> GB 0229578.0
 <151> 2002-12-19

<150> GB 0316989.3
 <151> 2003-07-21

<160> 16

<170> PatentIn version 3.4

<210> 1
 <211> 1266
 <212> DNA
 <213> *Euglena gracilis*

<220>
 <221> CDS
 <222> (1)..(1266)
 <223> delta-8-desaturase

<400> 1
 atg aag tca aag cgc caa gcg ctt ccc ctt aca att gat gga aca aca 48
 Met Lys Ser Lys Arg Gln Ala Leu Pro Leu Thr Ile Asp Gly Thr Thr
 1 5 10 15
 tat gat gtg tct gcc tgg gtc aat ttc cac cct ggt ggt gcg gaa att 96
 Tyr Asp Val Ser Ala Trp Val Asn Phe His Pro Gly Gly Ala Glu Ile
 20 25 30
 ata gag aat tac caa gga agg gat gcc act gat gcc ttc atg gtt atg 144
 Ile Glu Asn Tyr Gln Gly Arg Asp Ala Thr Asp Ala Phe Met Val Met
 35 40 45
 cac tct caa gaa gcc ttc gac aag ctc aag cgc atg ccc aaa atc aat 192
 His Ser Gln Glu Ala Phe Asp Lys Leu Lys Arg Met Pro Lys Ile Asn
 50 55 60

ccc agt tct gag ttg cca ccc cag gct gca gtg aat gaa gct caa gag	240
Pro Ser Ser Glu Leu Pro Pro Gln Ala Ala Val Asn Glu Ala Gln Glu	
65 70 75 80	
gat ttc cgg aag ctc cga gaa gag ttg atc gca act ggc atg ttt gat	288
Asp Phe Arg Lys Leu Arg Glu Glu Leu Ile Ala Thr Gly Met Phe Asp	
85 90 95	
gcc tcc ccc ctc tgg tac tca tac aaa atc agc acc aca ctg ggc ctt	336
Ala Ser Pro Leu Trp Tyr Ser Tyr Lys Ile Ser Thr Thr Leu Gly Leu	
100 105 110	
gga gtg ctg ggt tat ttc ctg atg gtt cag tat cag atg tat ttc att	384
Gly Val Leu Gly Tyr Phe Leu Met Val Gln Tyr Gln Met Tyr Phe Ile	
115 120 125	
ggg gca gtg ttg ctt ggg atg cac tat caa cag atg ggc tgg ctt tct	432
Gly Ala Val Leu Leu Gly Met His Tyr Gln Gln Met Gly Trp Leu Ser	
130 135 140	
cat gac att tgc cac cac cag act ttc aag aac cgg aac tgg aac aac	480
His Asp Ile Cys His His Gln Thr Phe Lys Asn Arg Asn Trp Asn Asn	
145 150 155 160	
ctc gtg gga ctg gta ttt ggc aat ggt ctg caa ggt ttt tcc gtg aca	528
Leu Val Gly Leu Val Phe Gly Asn Gly Leu Gln Gly Phe Ser Val Thr	
165 170 175	
tgc tgg aag gac aga cac aat gca cat cat tcg gca acc aat gtt caa	576
Cys Trp Lys Asp Arg His Asn Ala His His Ser Ala Thr Asn Val Gln	
180 185 190	
ggg cac gac cct gat att gac aac ctc ccc ctc tta gcc tgg tct gag	624
Gly His Asp Pro Asp Ile Asp Asn Leu Pro Leu Leu Ala Trp Ser Glu	
195 200 205	
gat gac gtc aca cgg gcg tca ccg att tcc cgc aag ctc att cag ttc	672
Asp Asp Val Thr Arg Ala Ser Pro Ile Ser Arg Lys Leu Ile Gln Phe	
210 215 220	
cag cag tat tat ttc ttg gtc atc tgt atc ttg ttg cgg ttc att tgg	720
Gln Gln Tyr Tyr Phe Leu Val Ile Cys Ile Leu Leu Arg Phe Ile Trp	
225 230 235 240	
tgt ttc cag agc gtg ttg acc gtg cgc agt ctg aag gac aga gat aac	768
Cys Phe Gln Ser Val Leu Thr Val Arg Ser Leu Lys Asp Arg Asp Asn	
245 250 255	
caa ttc tat cgc tct cag tat aag aag gag gcc att ggc ctc gcc ctg	816
Gln Phe Tyr Arg Ser Gln Tyr Lys Lys Glu Ala Ile Gly Leu Ala Leu	
260 265 270	
cat tgg aca ttg aag gcc ctg ttc cac tta ttc ttt atg ccc agc atc	864
His Trp Thr Leu Lys Ala Leu Phe His Leu Phe Phe Met Pro Ser Ile	
275 280 285	
ctc aca tcg ctg ttg gta ttt ttc gtt tcg gag ctg gtt ggc ggc ttc	912

Leu Thr Ser Leu Leu Val Phe Phe Val Ser Glu Leu Val Gly Gly Phe
 290 295 300
 ggc att gcg atc gtg gtg ttc atg aac cac tac cca ctg gag aag atc 960
 Gly Ile Ala Ile Val Val Phe Met Asn His Tyr Pro Leu Glu Lys Ile
 305 310 315 320
 ggg gac tcg gtc tgg gat ggc cat gga ttc tcg gtt ggc cag atc cat 1008
 Gly Asp Ser Val Trp Asp Gly His Gly Phe Ser Val Gly Gln Ile His
 325 330 335
 gag acc atg aac att cgg cga ggg att atc aca gat tgg ttt ttc gga 1056
 Glu Thr Met Asn Ile Arg Arg Gly Ile Ile Thr Asp Trp Phe Phe Gly
 340 345 350
 ggc ttg aac tac cag atc gag cac cat ttg tgg ccg acc ctc cct cgc 1104
 Gly Leu Asn Tyr Gln Ile Glu His His Leu Trp Pro Thr Leu Pro Arg
 355 360 365
 cac aac ctg aca gcg gtt agc tac cag gtg gaa cag ctg tgc cag aag 1152
 His Asn Leu Thr Ala Val Ser Tyr Gln Val Glu Gln Leu Cys Gln Lys
 370 375 380
 cac aac ctg ccg tat cgg aac ccg ctg ccc cat gaa ggg ttg gtc atc 1200
 His Asn Leu Pro Tyr Arg Asn Pro Leu Pro His Glu Gly Leu Val Ile
 385 390 395 400
 ctg ctg cgc tat ctg gcg gtg ttc gcc cgg atg gcg gag aag caa ccc 1248
 Leu Leu Arg Tyr Leu Ala Val Phe Ala Arg Met Ala Glu Lys Gln Pro
 405 410 415
 gcg ggg aag gct cta taa 1266
 Ala Gly Lys Ala Leu
 420

<210> 2

<211> 421

<212> PRT

<213> *Euglena gracilis*

<400> 2

Met Lys Ser Lys Arg Gln Ala Leu Pro Leu Thr Ile Asp Gly Thr Thr
 1 5 10 15

Tyr Asp Val Ser Ala Trp Val Asn Phe His Pro Gly Gly Ala Glu Ile
 20 25 30

Ile Glu Asn Tyr Gln Gly Arg Asp Ala Thr Asp Ala Phe Met Val Met
 35 40 45

His Ser Gln Glu Ala Phe Asp Lys Leu Lys Arg Met Pro Lys Ile Asn
 50 55 60

Pro Ser Ser Glu Leu Pro Pro Gln Ala Ala Val Asn Glu Ala Gln Glu
 65 70 75 80

Asp	Phe	Arg	Lys	Leu	Arg	Glu	Glu	Leu	Ile	Ala	Thr	Gly	Met	Phe	Asp	85	90	95
Ala	Ser	Pro	Leu	Trp	Tyr	Ser	Tyr	Lys	Ile	Ser	Thr	Thr	Leu	Gly	Leu	100	105	110
Gly	Val	Leu	Gly	Tyr	Phe	Leu	Met	Val	Gln	Tyr	Gln	Met	Tyr	Phe	Ile	115	120	125
Gly	Ala	Val	Leu	Leu	Gly	Met	His	Tyr	Gln	Gln	Met	Gly	Trp	Leu	Ser	130	135	140
His	Asp	Ile	Cys	His	His	Gln	Thr	Phe	Lys	Asn	Arg	Asn	Trp	Asn	Asn	145	150	155
Leu	Val	Gly	Leu	Val	Phe	Gly	Asn	Gly	Leu	Gln	Gly	Phe	Ser	Val	Thr	165	170	175
Cys	Trp	Lys	Asp	Arg	His	Asn	Ala	His	His	Ser	Ala	Thr	Asn	Val	Gln	180	185	190
Gly	His	Asp	Pro	Asp	Ile	Asp	Asn	Leu	Pro	Leu	Leu	Ala	Trp	Ser	Glu	195	200	205
Asp	Asp	Val	Thr	Arg	Ala	Ser	Pro	Ile	Ser	Arg	Lys	Leu	Ile	Gln	Phe	210	215	220
Gln	Gln	Tyr	Tyr	Phe	Leu	Val	Ile	Cys	Ile	Leu	Leu	Arg	Phe	Ile	Trp	225	230	235
Cys	Phe	Gln	Ser	Val	Leu	Thr	Val	Arg	Ser	Leu	Lys	Asp	Arg	Asp	Asn	245	250	255
Gln	Phe	Tyr	Arg	Ser	Gln	Tyr	Lys	Lys	Glu	Ala	Ile	Gly	Leu	Ala	Leu	260	265	270
His	Trp	Thr	Leu	Lys	Ala	Leu	Phe	His	Leu	Phe	Phe	Met	Pro	Ser	Ile	275	280	285
Leu	Thr	Ser	Leu	Leu	Val	Phe	Phe	Val	Ser	Glu	Leu	Val	Gly	Gly	Phe	290	295	300
Gly	Ile	Ala	Ile	Val	Val	Phe	Met	Asn	His	Tyr	Pro	Leu	Glu	Lys	Ile	305	310	315
Gly	Asp	Ser	Val	Trp	Asp	Gly	His	Gly	Phe	Ser	Val	Gly	Gln	Ile	His	325	330	335
Glu	Thr	Met	Asn	Ile	Arg	Arg	Gly	Ile	Ile	Thr	Asp	Trp	Phe	Phe	Gly	340	345	350
Gly	Leu	Asn	Tyr	Gln	Ile	Glu	His	His	Leu	Trp	Pro	Thr	Leu	Pro	Arg	355	360	365
His	Asn	Leu	Thr	Ala	Val	Ser	Tyr	Gln	Val	Glu	Gln	Leu	Cys	Gln	Lys	370	375	380

His Asn Leu Pro Tyr Arg Asn Pro Leu Pro His Glu Gly Leu Val Ile
 385 390 395 400

Leu Leu Arg Tyr Leu Ala Val Phe Ala Arg Met Ala Glu Lys Gln Pro
 405 410 415

Ala Gly Lys Ala Leu
 420

<210> 3

<211> 777

<212> DNA

<213> Isochrysis galbana

<220>

<221> CDS

<222> (1)..(777)

<223> delta-9-elongase

<400> 3

atg gcc ctc gca aac gac gcg gga gag cgc atc tgg gcg gct gtg acc 48
 Met Ala Leu Ala Asn Asp Ala Gly Glu Arg Ile Trp Ala Ala Val Thr
 1 5 10 15

gac ccg gaa atc ctc att ggc acc ttc tcg tac ttg cta ctc aaa ccg 96
 Asp Pro Glu Ile Leu Ile Gly Thr Phe Ser Tyr Leu Leu Leu Lys Pro
 20 25 30

ctg ctc cgc aat tcc ggg ctg gtg gat gag aag aag ggc gca tac agg 144
 Leu Leu Arg Asn Ser Gly Leu Val Asp Glu Lys Lys Gly Ala Tyr Arg
 35 40 45

acg tcc atg atc tgg tac aac gtt ctg ctg gcg ctc ttc tct gcg ctg 192
 Thr Ser Met Ile Trp Tyr Asn Val Leu Leu Ala Leu Phe Ser Ala Leu
 50 55 60

agc ttc tac gtg acg gcg acc gcc ctc ggc tgg gac tat ggt acg ggc 240
 Ser Phe Tyr Val Thr Ala Thr Ala Leu Gly Trp Asp Tyr Gly Thr Gly
 65 70 75 80

gcg tgg ctg cgc agg caa acc ggc gac aca ccg cag ccg ctc ttc cag 288
 Ala Trp Leu Arg Arg Gln Thr Gly Asp Thr Pro Gln Pro Leu Phe Gln
 85 90 95

tgc ccg tcc ccg gtt tgg gac tcg aag ctc ttc aca tgg acc gcc aag 336
 Cys Pro Ser Pro Val Trp Asp Ser Lys Leu Phe Thr Trp Thr Ala Lys
 100 105 110

gca ttc tat tac tcc aag tac gtg gag tac ctc gac acg gcc tgg ctg 384
 Ala Phe Tyr Tyr Ser Lys Tyr Val Glu Tyr Leu Asp Thr Ala Trp Leu
 115 120 125

agg gtc tcc ttt ctc cag gcc ttc cac cac ttt ggc gcg ccg tgg gat 432
 Arg Val Ser Phe Leu Gln Ala Phe His His Phe Gly Ala Pro Trp Asp
 130 135 140

gtg tac ctc ggc att cgg ctg cac aac gag ggc gta tgg atc ttc atg 480
 Val Tyr Leu Gly Ile Arg Leu His Asn Glu Gly Val Trp Ile Phe Met
 145 150 155 160

ttt ttc aac tcg ttc att cac acc atc atg tac acc tac tac ggc ctc 528
 Phe Phe Asn Ser Phe Ile His Thr Ile Met Tyr Thr Tyr Tyr Gly Leu
 165 170 175

acc gcc gcc ggg tat aag ttc aag gcc aag ccg ctc atc acc gcg atg 576
 Thr Ala Ala Gly Tyr Lys Phe Lys Ala Lys Pro Leu Ile Thr Ala Met
 180 185 190

cag atc tgc cag ttc gtg ggc ggc ttc ctg ttg gtc tgg gac tac atc 624
 Gln Ile Cys Gln Phe Val Gly Gly Phe Leu Leu Val Trp Asp Tyr Ile
 195 200 205

aac gtc ccc tgc ttc aac tcg gac aaa ggg aag ttg ttc agc tgg gct 672
 Asn Val Pro Cys Phe Asn Ser Asp Lys Gly Lys Leu Phe Ser Trp Ala
 210 215 220

ttc aac tat gca tac gtc ggc tcg gtc ttc ttg ctc ttc tgc cac ttt 720
 Phe Asn Tyr Ala Tyr Val Gly Ser Val Phe Leu Leu Phe Cys His Phe
 225 230 235 240

ttc tac cag gac aac ttg gca acg aag aaa tcg gcc aag gcg ggc aag 768
 Phe Tyr Gln Asp Asn Leu Ala Thr Lys Lys Ser Ala Lys Ala Gly Lys
 245 250 255

cag ctc tag 777
 Gln Leu

<210> 4

<211> 258

<212> PRT

<213> Isochrysis galbana

<400> 4

Met Ala Leu Ala Asn Asp Ala Gly Glu Arg Ile Trp Ala Ala Val Thr
 1 5 10 15

Asp Pro Glu Ile Leu Ile Gly Thr Phe Ser Tyr Leu Leu Leu Lys Pro
 20 25 30

Leu Leu Arg Asn Ser Gly Leu Val Asp Glu Lys Lys Gly Ala Tyr Arg
 35 40 45

Thr Ser Met Ile Trp Tyr Asn Val Leu Leu Ala Leu Phe Ser Ala Leu
 50 55 60

Ser Phe Tyr Val Thr Ala Thr Ala Leu Gly Trp Asp Tyr Gly Thr Gly
 65 70 75 80

Ala Trp Leu Arg Arg Gln Thr Gly Asp Thr Pro Gln Pro Leu Phe Gln
 85 90 95

Cys Pro Ser Pro Val Trp Asp Ser Lys Leu Phe Thr Trp Thr Ala Lys

100										105					110				
Ala	Phe	Tyr	Tyr	Ser	Lys	Tyr	Val	Glu	Tyr	Leu	Asp	Thr	Ala	Trp	Leu				
	115						120					125							
Arg	Val	Ser	Phe	Leu	Gln	Ala	Phe	His	His	Phe	Gly	Ala	Pro	Trp	Asp				
	130					135					140								
Val	Tyr	Leu	Gly	Ile	Arg	Leu	His	Asn	Glu	Gly	Val	Trp	Ile	Phe	Met				
145					150					155					160				
Phe	Phe	Asn	Ser	Phe	Ile	His	Thr	Ile	Met	Tyr	Thr	Tyr	Tyr	Gly	Leu				
				165					170					175					
Thr	Ala	Ala	Gly	Tyr	Lys	Phe	Lys	Ala	Lys	Pro	Leu	Ile	Thr	Ala	Met				
			180					185					190						
Gln	Ile	Cys	Gln	Phe	Val	Gly	Gly	Phe	Leu	Leu	Val	Trp	Asp	Tyr	Ile				
	195						200					205							
Asn	Val	Pro	Cys	Phe	Asn	Ser	Asp	Lys	Gly	Lys	Leu	Phe	Ser	Trp	Ala				
	210					215					220								
Phe	Asn	Tyr	Ala	Tyr	Val	Gly	Ser	Val	Phe	Leu	Leu	Phe	Cys	His	Phe				
225					230					235					240				
Phe	Tyr	Gln	Asp	Asn	Leu	Ala	Thr	Lys	Lys	Ser	Ala	Lys	Ala	Gly	Lys				
				245					250					255					

Gln Leu

<210> 5

<211> 1410

<212> DNA

<213> *Phaeodactylum tricornutum*

<220>

<221> CDS

<222> (1)..(1410)

<223> delta-5-desaturase

<400> 5

atg	gct	ccg	gat	gcg	gat	aag	ctt	cga	caa	cgc	cag	acg	act	gcg	gta	48
Met	Ala	Pro	Asp	Ala	Asp	Lys	Leu	Arg	Gln	Arg	Gln	Thr	Thr	Ala	Val	
1				5				10						15		

gcg	aag	cac	aat	gct	gct	acc	ata	tcg	acg	cag	gaa	cgc	ctt	tgc	agt	96
Ala	Lys	His	Asn	Ala	Ala	Thr	Ile	Ser	Thr	Gln	Glu	Arg	Leu	Cys	Ser	
			20					25					30			

ctg	tct	tcg	ctc	aaa	ggc	gaa	gaa	gtc	tgc	atc	gac	gga	atc	atc	tat	144
Leu	Ser	Ser	Leu	Lys	Gly	Glu	Glu	Val	Cys	Ile	Asp	Gly	Ile	Ile	Tyr	
			35				40					45				

gac	ctc	caa	tca	ttc	gat	cat	ccc	ggg	ggg	gaa	acg	atc	aaa	atg	ttt	192
Asp	Leu	Gln	Ser	Phe	Asp	His	Pro	Gly	Gly	Glu	Thr	Ile	Lys	Met	Phe	

50	55	60	
ggt ggc aac gat gtc act gta cag tac aag atg att cac ccg tac cat Gly Gly Asn Asp Val Thr Val Gln Tyr Lys Met Ile His Pro Tyr His 65 70 75 80	240		
acc gag aag cat ttg gaa aag atg aag cgt gtc ggc aag gtg acg gat Thr Glu Lys His Leu Glu Lys Met Lys Arg Val Gly Lys Val Thr Asp 85 90 95	288		
ttc gtc tgc gag tac aag ttc gat acc gaa ttt gaa cgc gaa atc aaa Phe Val Cys Glu Tyr Lys Phe Asp Thr Glu Phe Glu Arg Glu Ile Lys 100 105 110	336		
cga gaa gtc ttc aag att gtg cga cga ggc aag gat ttc ggt act ttg Arg Glu Val Phe Lys Ile Val Arg Arg Gly Lys Asp Phe Gly Thr Leu 115 120 125	384		
gga tgg ttc ttc cgt gcg ttt tgc tac att gcc att ttc ttc tac ctg Gly Trp Phe Phe Arg Ala Phe Cys Tyr Ile Ala Ile Phe Phe Tyr Leu 130 135 140	432		
cag tac cat tgg gtc acc acg gga acc tct tgg ctg ctg gcc gtg gcc Gln Tyr His Trp Val Thr Thr Gly Thr Ser Trp Leu Leu Ala Val Ala 145 150 155 160	480		
tac gga atc tcc caa gcg atg att ggc atg aat gtc cag cac gat gcc Tyr Gly Ile Ser Gln Ala Met Ile Gly Met Asn Val Gln His Asp Ala 165 170 175	528		
aac cac ggg gcc acc tcc aag cgt ccc tgg gtc aac gac atg cta ggc Asn His Gly Ala Thr Ser Lys Arg Pro Trp Val Asn Asp Met Leu Gly 180 185 190	576		
ctc ggt gcg gat ttt att ggt ggt tcc aag tgg ctc tgg cag gaa caa Leu Gly Ala Asp Phe Ile Gly Gly Ser Lys Trp Leu Trp Gln Glu Gln 195 200 205	624		
cac tgg acc cac cac gct tac acc aat cac gcc gag atg gat ccc gat His Trp Thr His His Ala Tyr Thr Asn His Ala Glu Met Asp Pro Asp 210 215 220	672		
agc ttt ggt gcc gaa cca atg ctc cta ttc aac gac tat ccc ttg gat Ser Phe Gly Ala Glu Pro Met Leu Leu Phe Asn Asp Tyr Pro Leu Asp 225 230 235 240	720		
cat ccc gct cgt acc tgg cta cat cgc ttt caa gca ttc ttt tac atg His Pro Ala Arg Thr Trp Leu His Arg Phe Gln Ala Phe Phe Tyr Met 245 250 255	768		
ccc gtc ttg gct gga tac tgg ttg tcc gct gtc ttc aat cca caa att Pro Val Leu Ala Gly Tyr Trp Leu Ser Ala Val Phe Asn Pro Gln Ile 260 265 270	816		
ctt gac ctc cag caa cgc ggc gca ctt tcc gtc ggt atc cgt ctc gac Leu Asp Leu Gln Gln Arg Gly Ala Leu Ser Val Gly Ile Arg Leu Asp 275 280 285	864		


```

aac gct ttc att cac tcg cga cgc aag tat gcg gtt ttc tgg cgg gct 912
Asn Ala Phe Ile His Ser Arg Arg Lys Tyr Ala Val Phe Trp Arg Ala
290 295 300

gtg tac att gcg gtg aac gtg att gct ccg ttt tac aca aac tcc ggc 960
Val Tyr Ile Ala Val Asn Val Ile Ala Pro Phe Tyr Thr Asn Ser Gly
305 310 315 320

ctc gaa tgg tcc tgg cgt gtc ttt gga aac atc atg ctc atg ggt gtg 1008
Leu Glu Trp Ser Trp Arg Val Phe Gly Asn Ile Met Leu Met Gly Val
325 330 335

gcg gaa tcg ctc gcg ctg gcg gtc ctg ttt tcg ttg tcg cac aat ttc 1056
Ala Glu Ser Leu Ala Leu Ala Val Leu Phe Ser Leu Ser His Asn Phe
340 345 350

gaa tcc gcg gat cgc gat ccg acc gcc cca ctg aaa aag acg gga gaa 1104
Glu Ser Ala Asp Arg Asp Pro Thr Ala Pro Leu Lys Lys Thr Gly Glu
355 360 365

cca gtc gac tgg ttc aag aca cag gtc gaa act tcc tgc act tac ggt 1152
Pro Val Asp Trp Phe Lys Thr Gln Val Glu Thr Ser Cys Thr Tyr Gly
370 375 380

gga ttc ctt tcc ggt tgc ttc acg gga ggt ctc aac ttt cag gtt gaa 1200
Gly Phe Leu Ser Gly Cys Phe Thr Gly Gly Leu Asn Phe Gln Val Glu
385 390 395 400

cac cac ttg ttc cca cgc atg agc agc gct tgg tat ccc tac att gcc 1248
His His Leu Phe Pro Arg Met Ser Ser Ala Trp Tyr Pro Tyr Ile Ala
405 410 415

ccc aag gtc cgc gaa att tgc gcc aaa cac ggc gtc cac tac gcc tac 1296
Pro Lys Val Arg Glu Ile Cys Ala Lys His Gly Val His Tyr Ala Tyr
420 425 430

tac ccg tgg atc cac caa aac ttt ctc tcc acc gtc cgc tac atg cac 1344
Tyr Pro Trp Ile His Gln Asn Phe Leu Ser Thr Val Arg Tyr Met His
435 440 445

gcg gcc ggg acc ggt gcc aac tgg cgc cag atg gcc aga gaa aat ccc 1392
Ala Ala Gly Thr Gly Ala Asn Trp Arg Gln Met Ala Arg Glu Asn Pro
450 455 460

ttg acc gga cgg gcg taa 1410
Leu Thr Gly Arg Ala
465

```

<210> 6

<211> 469

<212> PRT

<213> *Phaeodactylum tricornutum*

<400> 6

Met Ala Pro Asp Ala Asp Lys Leu Arg Gln Arg Gln Thr Thr Ala Val

1	5	10	15
Ala Lys His Asn Ala Ala Thr Ile Ser Thr Gln Glu Arg Leu Cys Ser	20	25	30
Leu Ser Ser Leu Lys Gly Glu Glu Val Cys Ile Asp Gly Ile Ile Tyr	35	40	45
Asp Leu Gln Ser Phe Asp His Pro Gly Gly Glu Thr Ile Lys Met Phe	50	55	60
Gly Gly Asn Asp Val Thr Val Gln Tyr Lys Met Ile His Pro Tyr His	65	70	75
Thr Glu Lys His Leu Glu Lys Met Lys Arg Val Gly Lys Val Thr Asp	85	90	95
Phe Val Cys Glu Tyr Lys Phe Asp Thr Glu Phe Glu Arg Glu Ile Lys	100	105	110
Arg Glu Val Phe Lys Ile Val Arg Arg Gly Lys Asp Phe Gly Thr Leu	115	120	125
Gly Trp Phe Phe Arg Ala Phe Cys Tyr Ile Ala Ile Phe Phe Tyr Leu	130	135	140
Gln Tyr His Trp Val Thr Thr Gly Thr Ser Trp Leu Leu Ala Val Ala	145	150	155
Tyr Gly Ile Ser Gln Ala Met Ile Gly Met Asn Val Gln His Asp Ala	165	170	175
Asn His Gly Ala Thr Ser Lys Arg Pro Trp Val Asn Asp Met Leu Gly	180	185	190
Leu Gly Ala Asp Phe Ile Gly Gly Ser Lys Trp Leu Trp Gln Glu Gln	195	200	205
His Trp Thr His His Ala Tyr Thr Asn His Ala Glu Met Asp Pro Asp	210	215	220
Ser Phe Gly Ala Glu Pro Met Leu Leu Phe Asn Asp Tyr Pro Leu Asp	225	230	235
His Pro Ala Arg Thr Trp Leu His Arg Phe Gln Ala Phe Phe Tyr Met	245	250	255
Pro Val Leu Ala Gly Tyr Trp Leu Ser Ala Val Phe Asn Pro Gln Ile	260	265	270
Leu Asp Leu Gln Gln Arg Gly Ala Leu Ser Val Gly Ile Arg Leu Asp	275	280	285
Asn Ala Phe Ile His Ser Arg Arg Lys Tyr Ala Val Phe Trp Arg Ala	290	295	300
Val Tyr Ile Ala Val Asn Val Ile Ala Pro Phe Tyr Thr Asn Ser Gly			

305 310 315 320
 Leu Glu Trp Ser Trp Arg Val Phe Gly Asn Ile Met Leu Met Gly Val
 325 330 335
 Ala Glu Ser Leu Ala Leu Ala Val Leu Phe Ser Leu Ser His Asn Phe
 340 345 350
 Glu Ser Ala Asp Arg Asp Pro Thr Ala Pro Leu Lys Lys Thr Gly Glu
 355 360 365
 Pro Val Asp Trp Phe Lys Thr Gln Val Glu Thr Ser Cys Thr Tyr Gly
 370 375 380
 Gly Phe Leu Ser Gly Cys Phe Thr Gly Gly Leu Asn Phe Gln Val Glu
 385 390 395 400
 His His Leu Phe Pro Arg Met Ser Ser Ala Trp Tyr Pro Tyr Ile Ala
 405 410 415
 Pro Lys Val Arg Glu Ile Cys Ala Lys His Gly Val His Tyr Ala Tyr
 420 425 430
 Tyr Pro Trp Ile His Gln Asn Phe Leu Ser Thr Val Arg Tyr Met His
 435 440 445
 Ala Ala Gly Thr Gly Ala Asn Trp Arg Gln Met Ala Arg Glu Asn Pro
 450 455 460
 Leu Thr Gly Arg Ala
 465

<210> 7
 <211> 1344
 <212> DNA
 <213> *Ceratodon purpureus*

<220>
 <221> CDS
 <222> (1)..(1344)
 <223> delta-5-desaturase

<400> 7
 atg gta tta cga gag caa gag cat gag cca ttc ttc att aaa att gat 48
 Met Val Leu Arg Glu Gln Glu His Glu Pro Phe Phe Ile Lys Ile Asp
 1 5 10 15
 gga aaa tgg tgt caa att gac gat gct gtc ctg aga tca cat cca ggt 96
 Gly Lys Trp Cys Gln Ile Asp Asp Ala Val Leu Arg Ser His Pro Gly
 20 25 30
 ggt agt gca att act acc tat aaa aat atg gat gcc act acc gta ttc 144
 Gly Ser Ala Ile Thr Thr Tyr Lys Asn Met Asp Ala Thr Thr Val Phe
 35 40 45
 cac aca ttc cat act ggt tct aaa gaa gcg tat caa tgg ctg aca gaa 192

His	Thr	Phe	His	Thr	Gly	Ser	Lys	Glu	Ala	Tyr	Gln	Trp	Leu	Thr	Glu		
50						55					60						
ttg	aaa	aaa	gag	tgc	cct	aca	caa	gaa	cca	gag	atc	cca	gat	att	aag	240	
Leu	Lys	Lys	Glu	Cys	Pro	Thr	Gln	Glu	Pro	Glu	Ile	Pro	Asp	Ile	Lys		
65					70					75					80		
gat	gac	cca	atc	aaa	gga	att	gat	gat	gtg	aac	atg	gga	act	ttc	aat	288	
Asp	Asp	Pro	Ile	Lys	Gly	Ile	Asp	Asp	Val	Asn	Met	Gly	Thr	Phe	Asn		
				85					90					95			
att	tct	gag	aaa	cga	tct	gcc	caa	ata	aat	aaa	agt	ttc	act	gat	cta	336	
Ile	Ser	Glu	Lys	Arg	Ser	Ala	Gln	Ile	Asn	Lys	Ser	Phe	Thr	Asp	Leu		
			100					105					110				
cgt	atg	cga	gtt	cgt	gca	gaa	gga	ctt	atg	gat	gga	tct	cct	ttg	ttc	384	
Arg	Met	Arg	Val	Arg	Ala	Glu	Gly	Leu	Met	Asp	Gly	Ser	Pro	Leu	Phe		
			115				120					125					
tac	att	aga	aaa	att	ctt	gaa	aca	atc	ttc	aca	att	ctt	ttt	gca	ttc	432	
Tyr	Ile	Arg	Lys	Ile	Leu	Glu	Thr	Ile	Phe	Thr	Ile	Leu	Phe	Ala	Phe		
	130					135					140						
tac	ctt	caa	tac	cac	aca	tat	tat	ctt	cca	tca	gct	att	cta	atg	gga	480	
Tyr	Leu	Gln	Tyr	His	Thr	Tyr	Tyr	Leu	Pro	Ser	Ala	Ile	Leu	Met	Gly		
145					150					155					160		
gtt	gcg	tggt	caa	caa	ttg	gga	tggt	tta	atc	cat	gaa	ttc	gca	cat	cat	528	
Val	Ala	Trp	Gln	Gln	Leu	Gly	Trp	Leu	Ile	His	Glu	Phe	Ala	His	His		
				165					170					175			
cag	ttg	ttc	aaa	aac	aga	tac	tac	aat	gat	ttg	gcc	agc	tat	ttc	gtt	576	
Gln	Leu	Phe	Lys	Asn	Arg	Tyr	Tyr	Asn	Asp	Leu	Ala	Ser	Tyr	Phe	Val		
			180					185					190				
gga	aac	ttt	tta	caa	gga	ttc	tca	tct	ggt	ggt	tggt	aaa	gag	cag	cac	624	
Gly	Asn	Phe	Leu	Gln	Gly	Phe	Ser	Ser	Gly	Gly	Trp	Lys	Glu	Gln	His		
		195					200					205					
aat	gtg	cat	cac	gca	gcc	aca	aat	gtt	gtt	gga	cga	gac	gga	gat	ctt	672	
Asn	Val	His	His	Ala	Ala	Thr	Asn	Val	Val	Gly	Arg	Asp	Gly	Asp	Leu		
	210					215					220						
gat	tta	gtc	cca	ttc	tat	gct	aca	gtg	gca	gaa	cat	ctc	aac	aat	tat	720	
Asp	Leu	Val	Pro	Phe	Tyr	Ala	Thr	Val	Ala	Glu	His	Leu	Asn	Asn	Tyr		
225					230					235					240		
tct	cag	gat	tca	tggt	gtt	atg	act	cta	ttc	aga	tggt	caa	cat	gtt	cat	768	
Ser	Gln	Asp	Ser	Trp	Val	Met	Thr	Leu	Phe	Arg	Trp	Gln	His	Val	His		
				245					250					255			
tggt	aca	ttc	atg	tta	cca	ttc	ctc	cgt	ctc	tcgt	tggt	ctt	ctt	cag	tca	816	
Trp	Thr	Phe	Met	Leu	Pro	Phe	Leu	Arg	Leu	Ser	Trp	Leu	Leu	Gln	Ser		
			260					265					270				
atc	att	ttt	gtt	agt	cag	atg	cca	act	cat	tat	tat	gac	tat	tac	aga	864	
Ile	Ile	Phe	Val	Ser	Gln	Met	Pro	Thr	His	Tyr	Tyr	Asp	Tyr	Tyr	Arg		

275					280					285					
aat act gcg att tat gaa cag gtt ggt ctc tct ttg cac tgg gct tgg	912														
Asn Thr Ala Ile Tyr Glu Gln Val Gly Leu Ser Leu His Trp Ala Trp															
290 295 300															
tca ttg ggt caa ttg tat ttc cta ccc gat tgg tca act aga ata atg	960														
Ser Leu Gly Gln Leu Tyr Phe Leu Pro Asp Trp Ser Thr Arg Ile Met															
305 310 315 320															
ttc ttc ctt gtt tct cat ctt gtt gga ggt ttc ctg ctc tct cat gta	1008														
Phe Phe Leu Val Ser His Leu Val Gly Gly Phe Leu Leu Ser His Val															
325 330 335															
gtt act ttc aat cat tat tca gtg gag aag ttt gca ttg agc tcg aac	1056														
Val Thr Phe Asn His Tyr Ser Val Glu Lys Phe Ala Leu Ser Ser Asn															
340 345 350															
atc atg tca aat tac gct tgt ctt caa atc atg acc aca aga aat atg	1104														
Ile Met Ser Asn Tyr Ala Cys Leu Gln Ile Met Thr Thr Arg Asn Met															
355 360 365															
aga cct gga aga ttc att gac tgg ctt tgg gga ggt ctt aac tat cag	1152														
Arg Pro Gly Arg Phe Ile Asp Trp Leu Trp Gly Gly Leu Asn Tyr Gln															
370 375 380															
att gag cac cat ctt ttc cca acg atg cca cga cac aac ttg aac act	1200														
Ile Glu His His Leu Phe Pro Thr Met Pro Arg His Asn Leu Asn Thr															
385 390 395 400															
gtt atg cca ctt gtt aag gag ttt gca gca gca aat ggt tta cca tac	1248														
Val Met Pro Leu Val Lys Glu Phe Ala Ala Ala Asn Gly Leu Pro Tyr															
405 410 415															
atg gtc gac gat tat ttc aca gga ttc tgg ctt gaa att gag caa ttc	1296														
Met Val Asp Asp Tyr Phe Thr Gly Phe Trp Leu Glu Ile Glu Gln Phe															
420 425 430															
cga aat att gca aat gtt gct gct aaa ttg act aaa aag att gcc tag	1344														
Arg Asn Ile Ala Asn Val Ala Ala Lys Leu Thr Lys Lys Ile Ala															
435 440 445															
<210> 8															
<211> 447															
<212> PRT															
<213> Ceratodon purpureus															
<400> 8															
Met Val Leu Arg Glu Gln Glu His Glu Pro Phe Phe Ile Lys Ile Asp															
1 5 10 15															
Gly Lys Trp Cys Gln Ile Asp Asp Ala Val Leu Arg Ser His Pro Gly															
20 25 30															
Gly Ser Ala Ile Thr Thr Tyr Lys Asn Met Asp Ala Thr Thr Val Phe															
35 40 45															

His	Thr	Phe	His	Thr	Gly	Ser	Lys	Glu	Ala	Tyr	Gln	Trp	Leu	Thr	Glu	50	55	60
Leu	Lys	Lys	Glu	Cys	Pro	Thr	Gln	Glu	Pro	Glu	Ile	Pro	Asp	Ile	Lys	65	70	75
Asp	Asp	Pro	Ile	Lys	Gly	Ile	Asp	Asp	Val	Asn	Met	Gly	Thr	Phe	Asn	85	90	95
Ile	Ser	Glu	Lys	Arg	Ser	Ala	Gln	Ile	Asn	Lys	Ser	Phe	Thr	Asp	Leu	100	105	110
Arg	Met	Arg	Val	Arg	Ala	Glu	Gly	Leu	Met	Asp	Gly	Ser	Pro	Leu	Phe	115	120	125
Tyr	Ile	Arg	Lys	Ile	Leu	Glu	Thr	Ile	Phe	Thr	Ile	Leu	Phe	Ala	Phe	130	135	140
Tyr	Leu	Gln	Tyr	His	Thr	Tyr	Tyr	Leu	Pro	Ser	Ala	Ile	Leu	Met	Gly	145	150	155
Val	Ala	Trp	Gln	Gln	Leu	Gly	Trp	Leu	Ile	His	Glu	Phe	Ala	His	His	165	170	175
Gln	Leu	Phe	Lys	Asn	Arg	Tyr	Tyr	Asn	Asp	Leu	Ala	Ser	Tyr	Phe	Val	180	185	190
Gly	Asn	Phe	Leu	Gln	Gly	Phe	Ser	Ser	Gly	Gly	Trp	Lys	Glu	Gln	His	195	200	205
Asn	Val	His	His	Ala	Ala	Thr	Asn	Val	Val	Gly	Arg	Asp	Gly	Asp	Leu	210	215	220
Asp	Leu	Val	Pro	Phe	Tyr	Ala	Thr	Val	Ala	Glu	His	Leu	Asn	Asn	Tyr	225	230	235
Ser	Gln	Asp	Ser	Trp	Val	Met	Thr	Leu	Phe	Arg	Trp	Gln	His	Val	His	245	250	255
Trp	Thr	Phe	Met	Leu	Pro	Phe	Leu	Arg	Leu	Ser	Trp	Leu	Leu	Gln	Ser	260	265	270
Ile	Ile	Phe	Val	Ser	Gln	Met	Pro	Thr	His	Tyr	Tyr	Asp	Tyr	Tyr	Arg	275	280	285
Asn	Thr	Ala	Ile	Tyr	Glu	Gln	Val	Gly	Leu	Ser	Leu	His	Trp	Ala	Trp	290	295	300
Ser	Leu	Gly	Gln	Leu	Tyr	Phe	Leu	Pro	Asp	Trp	Ser	Thr	Arg	Ile	Met	305	310	315
Phe	Phe	Leu	Val	Ser	His	Leu	Val	Gly	Gly	Phe	Leu	Leu	Ser	His	Val	325	330	335
Val	Thr	Phe	Asn	His	Tyr	Ser	Val	Glu	Lys	Phe	Ala	Leu	Ser	Ser	Asn	340	345	350

Ile Met Ser Asn Tyr Ala Cys Leu Gln Ile Met Thr Thr Arg Asn Met
 355 360 365

Arg Pro Gly Arg Phe Ile Asp Trp Leu Trp Gly Gly Leu Asn Tyr Gln
 370 375 380

Ile Glu His His Leu Phe Pro Thr Met Pro Arg His Asn Leu Asn Thr
 385 390 395 400

Val Met Pro Leu Val Lys Glu Phe Ala Ala Ala Asn Gly Leu Pro Tyr
 405 410 415

Met Val Asp Asp Tyr Phe Thr Gly Phe Trp Leu Glu Ile Glu Gln Phe
 420 425 430

Arg Asn Ile Ala Asn Val Ala Ala Lys Leu Thr Lys Lys Ile Ala
 435 440 445

<210> 9
 <211> 1443
 <212> DNA
 <213> Physcomitrella patens

<220>
 <221> CDS
 <222> (1)..(1443)
 <223> delta-5-desaturase

<220>
 <221> misc_feature
 <222> (317)..(317)
 <223> k is g or t/u

<220>
 <221> misc_feature
 <222> (361)..(361)
 <223> r is g or a

<400> 9
 atg gcg ccc cac tct gcg gat act gct ggg ctc gtg cct tct gac gaa 48
 Met Ala Pro His Ser Ala Asp Thr Ala Gly Leu Val Pro Ser Asp Glu
 1 5 10 15

ttg agg cta cga acg tcg aat tca aag ggt ccc gaa caa gag caa act 96
 Leu Arg Leu Arg Thr Ser Asn Ser Lys Gly Pro Glu Gln Glu Gln Thr
 20 25 30

ttg aag aag tac acc ctt gaa gat gtc agc cgc cac aac acc cca gca 144
 Leu Lys Lys Tyr Thr Leu Glu Asp Val Ser Arg His Asn Thr Pro Ala
 35 40 45

gat tgt tgg ttg gtg ata tgg ggc aaa gtc tac gat gtc aca agc tgg 192
 Asp Cys Trp Leu Val Ile Trp Gly Lys Val Tyr Asp Val Thr Ser Trp
 50 55 60

att ccc aat cat ccg ggg ggc agt ctc atc cac gta aaa gca ggg cag	240
Ile Pro Asn His Pro Gly Gly Ser Leu Ile His Val Lys Ala Gly Gln	
65 70 75 80	
gat tcc act cag ctt ttc gat tcc tat cac ccc ctt tat gtc agg aaa	288
Asp Ser Thr Gln Leu Phe Asp Ser Tyr His Pro Leu Tyr Val Arg Lys	
85 90 95	
atg ctc gcg aag tac tgt att ggg gaa tka gta ccg tct gct ggt gat	336
Met Leu Ala Lys Tyr Cys Ile Gly Glu Xaa Val Pro Ser Ala Gly Asp	
100 105 110	
gac aag ttt aag aaa gca act ctg rag tat gca gat gcc gaa aat gaa	384
Asp Lys Phe Lys Lys Ala Thr Leu Xaa Tyr Ala Asp Ala Glu Asn Glu	
115 120 125	
gat ttc tat ttg gtt gtg aag caa cga gtt gaa tct tat ttc aag agt	432
Asp Phe Tyr Leu Val Val Lys Gln Arg Val Glu Ser Tyr Phe Lys Ser	
130 135 140	
aac aag ata aac ccc caa att cat cca cat atg atc ctg aag tca ttg	480
Asn Lys Ile Asn Pro Gln Ile His Pro His Met Ile Leu Lys Ser Leu	
145 150 155 160	
ttc att ctt ggg gga tat ttc gcc agt tac tat tta gcg ttc ttc tgg	528
Phe Ile Leu Gly Gly Tyr Phe Ala Ser Tyr Tyr Leu Ala Phe Phe Trp	
165 170 175	
tct tca agt gtc ctt gtt tct ttg ttt ttc gca ttg tgg atg ggg ttc	576
Ser Ser Ser Val Leu Val Ser Leu Phe Phe Ala Leu Trp Met Gly Phe	
180 185 190	
ttc gca gcg gaa gtc ggc gtg tcg att caa cat gat gga aat cat ggt	624
Phe Ala Ala Glu Val Gly Val Ser Ile Gln His Asp Gly Asn His Gly	
195 200 205	
tca tac act aaa tgg cgt ggc ttt gga tat atc atg gga gcc tcc cta	672
Ser Tyr Thr Lys Trp Arg Gly Phe Gly Tyr Ile Met Gly Ala Ser Leu	
210 215 220	
gat cta gtc gga gcc agt agc ttc atg tgg aga cag caa cac gtt gtg	720
Asp Leu Val Gly Ala Ser Ser Phe Met Trp Arg Gln Gln His Val Val	
225 230 235 240	
gga cat cac tcg ttt aca aat gtg gac aac tac gat cct gat att cgt	768
Gly His His Ser Phe Thr Asn Val Asp Asn Tyr Asp Pro Asp Ile Arg	
245 250 255	
gtg aaa gat cca gat gtc agg agg gtt gcg acc aca caa cca aga caa	816
Val Lys Asp Pro Asp Val Arg Arg Val Ala Thr Thr Gln Pro Arg Gln	
260 265 270	
tgg tat cat gcg tat cag cat atc tac ctg gca gta tta tat gga act	864
Trp Tyr His Ala Tyr Gln His Ile Tyr Leu Ala Val Leu Tyr Gly Thr	
275 280 285	
cta gct ctt aag agt att ttt cta gat gat ttc ctt gcg tac ttc aca	912

Leu	Ala	Leu	Lys	Ser	Ile	Phe	Leu	Asp	Asp	Phe	Leu	Ala	Tyr	Phe	Thr		
290						295					300						
gga	tca	att	ggc	cct	gtc	aag	gtg	gcg	aaa	atg	acc	ccc	ctg	gag	ttc	960	
Gly	Ser	Ile	Gly	Pro	Val	Lys	Val	Ala	Lys	Met	Thr	Pro	Leu	Glu	Phe		
305					310					315					320		
aac	atc	ttc	ttt	cag	gga	aag	ctg	cta	tat	gcg	ttc	tac	atg	ttc	gtg	1008	
Asn	Ile	Phe	Phe	Gln	Gly	Lys	Leu	Leu	Tyr	Ala	Phe	Tyr	Met	Phe	Val		
				325					330					335			
ttg	cca	tct	gtg	tac	ggg	gtt	cac	tcc	gga	gga	act	ttc	ttg	gca	cta	1056	
Leu	Pro	Ser	Val	Tyr	Gly	Val	His	Ser	Gly	Gly	Thr	Phe	Leu	Ala	Leu		
			340					345					350				
tat	gtg	gct	tct	cag	ctc	att	aca	ggg	tgg	atg	tta	gct	ttt	ctt	ttt	1104	
Tyr	Val	Ala	Ser	Gln	Leu	Ile	Thr	Gly	Trp	Met	Leu	Ala	Phe	Leu	Phe		
		355					360					365					
caa	gta	gca	cat	gtc	gtg	gat	gat	gtt	gca	ttt	cct	aca	cca	gaa	ggg	1152	
Gln	Val	Ala	His	Val	Val	Asp	Asp	Val	Ala	Phe	Pro	Thr	Pro	Glu	Gly		
	370					375					380						
ggg	aag	gtg	aag	gga	gga	tgg	gct	gca	atg	cag	gtt	gca	aca	act	acg	1200	
Gly	Lys	Val	Lys	Gly	Gly	Trp	Ala	Ala	Met	Gln	Val	Ala	Thr	Thr	Thr		
385					390					395					400		
gat	ttc	agt	cca	cgc	tca	tgg	ttc	tgg	ggg	cat	gtc	tct	gga	gga	tta	1248	
Asp	Phe	Ser	Pro	Arg	Ser	Trp	Phe	Trp	Gly	His	Val	Ser	Gly	Gly	Leu		
				405					410					415			
aac	aac	caa	att	gag	cat	cat	ctg	ttt	cca	gga	gtg	tgc	cat	gtt	cat	1296	
Asn	Asn	Gln	Ile	Glu	His	His	Leu	Phe	Pro	Gly	Val	Cys	His	Val	His		
			420					425					430				
tat	cca	gcc	att	cag	cct	att	gtc	gag	aag	acg	tgc	aag	gaa	ttc	gat	1344	
Tyr	Pro	Ala	Ile	Gln	Pro	Ile	Val	Glu	Lys	Thr	Cys	Lys	Glu	Phe	Asp		
		435					440					445					
gtg	cct	tat	gta	gcc	tac	cca	act	ttt	tgg	act	gcg	ttg	aga	gcc	cac	1392	
Val	Pro	Tyr	Val	Ala	Tyr	Pro	Thr	Phe	Trp	Thr	Ala	Leu	Arg	Ala	His		
	450					455					460						
ttt	gcg	cat	ttg	aaa	aag	gtt	gga	ttg	aca	gag	ttt	cgg	ctc	gat	ggc	1440	
Phe	Ala	His	Leu	Lys	Lys	Val	Gly	Leu	Thr	Glu	Phe	Arg	Leu	Asp	Gly		
465					470					475					480		
tga																1443	

<210> 10

<211> 480

<212> PRT

<213> Physcomitrella patens

<220>

<221> misc_feature
 <222> (106)..(106)
 <223> Xaa is unknown or other

<220>
 <221> misc_feature
 <222> (121)..(121)
 <223> Xaa is unknown or other

<400> 10

Met	Ala	Pro	His	Ser	Ala	Asp	Thr	Ala	Gly	Leu	Val	Pro	Ser	Asp	Glu	1	5	10	15
Leu	Arg	Leu	Arg	Thr	Ser	Asn	Ser	Lys	Gly	Pro	Glu	Gln	Glu	Gln	Thr	20	25	30	
Leu	Lys	Lys	Tyr	Thr	Leu	Glu	Asp	Val	Ser	Arg	His	Asn	Thr	Pro	Ala	35	40	45	
Asp	Cys	Trp	Leu	Val	Ile	Trp	Gly	Lys	Val	Tyr	Asp	Val	Thr	Ser	Trp	50	55	60	
Ile	Pro	Asn	His	Pro	Gly	Gly	Ser	Leu	Ile	His	Val	Lys	Ala	Gly	Gln	65	70	75	80
Asp	Ser	Thr	Gln	Leu	Phe	Asp	Ser	Tyr	His	Pro	Leu	Tyr	Val	Arg	Lys	85	90	95	
Met	Leu	Ala	Lys	Tyr	Cys	Ile	Gly	Glu	Xaa	Val	Pro	Ser	Ala	Gly	Asp	100	105	110	
Asp	Lys	Phe	Lys	Lys	Ala	Thr	Leu	Xaa	Tyr	Ala	Asp	Ala	Glu	Asn	Glu	115	120	125	
Asp	Phe	Tyr	Leu	Val	Val	Lys	Gln	Arg	Val	Glu	Ser	Tyr	Phe	Lys	Ser	130	135	140	
Asn	Lys	Ile	Asn	Pro	Gln	Ile	His	Pro	His	Met	Ile	Leu	Lys	Ser	Leu	145	150	155	160
Phe	Ile	Leu	Gly	Gly	Tyr	Phe	Ala	Ser	Tyr	Tyr	Leu	Ala	Phe	Phe	Trp	165	170	175	
Ser	Ser	Ser	Val	Leu	Val	Ser	Leu	Phe	Phe	Ala	Leu	Trp	Met	Gly	Phe	180	185	190	
Phe	Ala	Ala	Glu	Val	Gly	Val	Ser	Ile	Gln	His	Asp	Gly	Asn	His	Gly	195	200	205	
Ser	Tyr	Thr	Lys	Trp	Arg	Gly	Phe	Gly	Tyr	Ile	Met	Gly	Ala	Ser	Leu	210	215	220	
Asp	Leu	Val	Gly	Ala	Ser	Ser	Phe	Met	Trp	Arg	Gln	Gln	His	Val	Val	225	230	235	240
Gly	His	His	Ser	Phe	Thr	Asn	Val	Asp	Asn	Tyr	Asp	Pro	Asp	Ile	Arg	245	250	255	

Val Lys Asp Pro Asp Val Arg Arg Val Ala Thr Thr Gln Pro Arg Gln
 260 265 270
 Trp Tyr His Ala Tyr Gln His Ile Tyr Leu Ala Val Leu Tyr Gly Thr
 275 280 285
 Leu Ala Leu Lys Ser Ile Phe Leu Asp Asp Phe Leu Ala Tyr Phe Thr
 290 295 300
 Gly Ser Ile Gly Pro Val Lys Val Ala Lys Met Thr Pro Leu Glu Phe
 305 310 315 320
 Asn Ile Phe Phe Gln Gly Lys Leu Leu Tyr Ala Phe Tyr Met Phe Val
 325 330 335
 Leu Pro Ser Val Tyr Gly Val His Ser Gly Gly Thr Phe Leu Ala Leu
 340 345 350
 Tyr Val Ala Ser Gln Leu Ile Thr Gly Trp Met Leu Ala Phe Leu Phe
 355 360 365
 Gln Val Ala His Val Val Asp Asp Val Ala Phe Pro Thr Pro Glu Gly
 370 375 380
 Gly Lys Val Lys Gly Gly Trp Ala Ala Met Gln Val Ala Thr Thr Thr
 385 390 395 400
 Asp Phe Ser Pro Arg Ser Trp Phe Trp Gly His Val Ser Gly Gly Leu
 405 410 415
 Asn Asn Gln Ile Glu His His Leu Phe Pro Gly Val Cys His Val His
 420 425 430
 Tyr Pro Ala Ile Gln Pro Ile Val Glu Lys Thr Cys Lys Glu Phe Asp
 435 440 445
 Val Pro Tyr Val Ala Tyr Pro Thr Phe Trp Thr Ala Leu Arg Ala His
 450 455 460
 Phe Ala His Leu Lys Lys Val Gly Leu Thr Glu Phe Arg Leu Asp Gly
 465 470 475 480

<210> 11
 <211> 29
 <212> DNA
 <213> Artificial sequence

<220>
 <223> Primer EDELTA8BamF

<400> 11
 atggatccac catgaagtca aagcgccaa

<210> 12

<211> 26
 <212> DNA
 <213> Artificial sequence

<220>
 <223> Primer EDELTA8XhoR

<400> 12
 atctcgagtt atagagcctt ccccg

26

<210> 13
 <211> 25
 <212> PRT
 <213> Artificial sequence

<220>
 <223> The first 25 amino acid residues of LARS delta-8-desaturase

<400> 13

Met Lys Ser Lys Arg Gln Ala Leu Pro Leu Thr Ile Asp Gly Thr Thr
 1 5 10 15

Tyr Asp Val Ser Ala Trp Val Asn Phe
 20 25

<210> 14
 <211> 25
 <212> PRT
 <213> Artificial sequence

<220>
 <223> The first 25 amino acid residues of delta-8-desaturase described
 by Wallis & Browne (ABB 1999)

<400> 14

Met Lys Ser Lys Arg Gln Ala Leu Ser Pro Leu Gln Leu Met Glu Gln
 1 5 10 15

Thr Tyr Asp Val Ser Ala Trp Val Asn
 20 25

<210> 15
 <211> 24
 <212> PRT
 <213> Artificial sequence

<220>
 <223> The first 25 amino acid residues of delta-8-desaturase as given
 in GenBank AAD45877

<400> 15

Met Lys Ser Lys Arg Gln Ala Leu Ser Pro Leu Gln Leu Met Glu Gln
1 5 10 15

Thr Tyr Asp Val Val Asn Phe His
 20

<210> 16

<211> 60

<212> DNA

<213> Artificial sequence

<220>

<223> Primer

<400> 16

gtcgaccgcg ggactagtgg gccctctaga cccgggggat ccggatctgc tggctatgaa 60